

## Sequence Listing

<11> Genentech, Inc. and Novartis Corporation

<12> NOVEL POLYESTERS, THEIR NUCLEIC ACIDS, AND METHOD FOR THEIR USE IN ANTIGENICITY AND VACCINIZATION

<13> 11/16/92/PT

<141> 25/10-10-95

<150> US 60/108,587

<151> 1999-10-07

<152> US 60/162,611

<153> 1999-10-28

<160> 29

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<212> DNA

<213> Homo sapiens

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gcc gcc aag gtg ctg ctg gac gac acg gtg cgg ctg aca 128  
Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr  
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gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167  
Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr  
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gaa tat att att cga gtg caa aga gga att tct gtg gaa 206  
Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu  
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Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp  
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cat att cgt gcc aat aat ttg att ggt aac atg gat cgt 323  
Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg  
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gaa ttc ata ggt gaa agg cag aac atc ctt cag aac tat 362  
Glu Phe Ile Ala Glu Arg Gln Lys Gly Leu Gln Asn Tyr  
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Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys  
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			285				290						
70	111	111	111	111	111	111	111	111	111	111	111	111	986
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	295				300						305		
75	111	111	111	111	111	111	111	111	111	111	111	111	1025
	Asn	Ser	Leu	Leu	Gly	Leu	Pro	Ser	Phe	Tyr	Arg	Ser	Tyr
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Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr  
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235 240

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265 270

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275 280 285

Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr  
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290 295 300

Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser  
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310 315

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25	Gly	Ser	Gln	Gln	Gln	Arg	Lys	Lys	Arg	Lys	Ile	Leu	Ala	Arg	Lys		600
	Lys	Ser	Lys	Arg	Ser	Ala	Leu	Gln	Asn	Ser	Gln	Gln	His	Ser	Ala		620
30	Arg	Tyr	Ser	Asn	Ser	Asn	Asn	Ser	Gly	Ser	Gly	Ala	Ser	Ser	Pro		640
	Leu	Thr	Ser	Pro	Ser	Ser	Pro	Thr	Pro	Pro	Ser	Thr	Ser	Gly	Ile		660
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	Pro	Leu	Pro	Pro	Ala	Ser	Thr	Gln	Val	Pro	Ala	Gln	Leu	Ser	Ser		700
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Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg  
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Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn  
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Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr  
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Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met  
 65 70

Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu  
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Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro  
 90 95 100

Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly  
 105 110

Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser  
 115 120 125

Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu  
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Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu  
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10	241	251	261	271	281	291	301	311	321	331	341	351	361	371
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15	381	391	401	411	421	431	441	451	461	471	481	491	501	511
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	Met Ser Val Arg Leu Val Lys Lys Thr Gly Asn His Arg His Thr	114	115
10	Asn Gly Ser Phe His Ser Arg Lys Lys Lys Ala Leu Thr Thr Lys	116	117
	Pro Phe Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu	118	119
15	Lys Leu Glu Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Phe Glu	120	121
	Ala Gly Lys Glu His Glu Pro Cys Arg Pro Ile Gly Thr Pro Ser	122	123
20	Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Glu Pro Ser Lys Met	124	125
	Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe	126	127
25	Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn	128	129
30	Lys Leu Ser Ser Val Val Pro Ser Val Tyr Lys Asn Leu Val Pro	130	131
	Lys Pro Val Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn	132	133
35	Arg Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu Ser	134	135
	Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val Val Leu Ala	136	137
40	Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu Ser Pro Ser Ser Thr	138	139
45	Thr Pro Pro Ile Glu Ile Ser Ser Ser Arg Leu Thr Lys Leu Thr	140	141
	Arg Arg Thr Thr Asp Arg Lys Ser Glu Phe Leu Lys Thr Leu Lys	142	143
50	Arg Asp Arg Asn Gly Asp Thr Ser Glu Asn Arg Asp Cys Arg Lys	144	145
55	Leu Glu Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn	146	147
	Gly Glu Glu Gly Lys His Glu Asn Gly Leu Ala Leu Pro Val Val	148	149
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 aagcctgtac cacctccttc caagcctaatt gcatggaaag ctaacaggat 350  
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 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Ile Leu Ile  
 334 340 346



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 aatacttttt atgttccctt tcccccttcc ccccttttcc ctttccccct 200  
 ttggaaacgt gtcaggaacc aaatagttaa agatgagcag ttgaggggac 250  
 tgagagagtg atcgacacag aacctggctt ctctgtgctt catcataagt 300  
 cgtgctgccg gccaggttac ttaagcacc ttttaacaag gaaaccttgt 350  
 gggagatcca gctggccgac tcgagttcag aaacaggacc acagaggtta 400  
 cactctggga tccctggccat gaggttggat gcctcacctt actgaaagga 450  
 gacactggac ctaa atg gcg cag cat gat ttt gtt cct gct 491  
 Met Ala Gln His Asp Phe Val Pro Ala  
 1 5

tgg cta aat ttc tca aca cca cag tca gct aag tca cct 530  
 Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro  
 10 15 20

act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 565  
 Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg  
 25 30 35

gga gaa ggt aga ttt gga gta agc cgc cgt cga cat aat 600  
 Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn  
 40 45

tcc tct gat ggt ttt ttt aac aat ggt ccc cta cga act 647  
 Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr  
 50 55 60

gca gga gat tct tgg cac cag ccc tcc tgt tcc gcc atg 686  
 Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met  
 65 70

att ctg tgg act ctg gtg tct cta agg gag cat atg ctg 725  
 Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu

75

80

85

gaa tca cag gga acc cat ctg gtt ggc ata gct ctt ccc 764  
 Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro  
           90                          95                  100

cga ggt cat gat ggc atg agc caa cgt agt gta ggt ggc 803  
 Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly  
                   105                          110

aca ggg aac cat cgc cat tgg aat ggc agc ttc cac tcc 842  
 Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser  
           115                          120                  125

cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag 881  
 Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu  
                   130                          135

att agg gaa gaa aag aaa gaa gac aag gtg gaa aag ttg 920  
 Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu  
           140                          145                  150

cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa 959  
 Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu  
                   155                          160                  165

gct ggc aaa cag cat cag cca tgc aga cct att ggg aca 998  
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr  
                   170                          175

cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa 1037  
 Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln  
           180                          185                  190

ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag 1076  
 Pro Ser Lys Met Leu Val Ile Lys Lys Val Ser Lys Glu  
                   195                          200

gat cct gct gct gcc ttc tct gct gca ttc acc tca cca 1115  
 Asp Pro Ala Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro  
           205                          210                  215

gga tct cac cat gca aat ggg aac aaa ttg tca tcc gtg 1154  
 Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val  
                   220                          225                  230

gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta 1193  
 Val Pro Ser Val Tyr Lys Asn Leu Val Pro Lys Pro Val  
                   235                          240

cca cct cct tcc aag cct aat gca tgg aaa gct aac agg 1232  
 Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn Arg  
           245                          250                  255

atg gag cac aag tca gga tcc ctt tcc tct agc cgg gag 1271  
 Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu  
                   260                          265

tct gct ttt acc agt cca atc tcc gtt acc aaa cca gtg 1310  
 Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val  
           270                          275                  280

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349  
 Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu  
           285                          290                          295

agt ccc tcc agc acc acc cct cca att gag atc agc tcc 1388  
 Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser  
                           300                          305

tct cgt ctg acc aag ttg acc cgc cga acc acc gac agg 1427  
 Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg  
           310                          315                          320

aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466  
 Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn  
                           325                          330

gga gac ttc tca gag aat aga gac tgt gac aag ctg gaa 1505  
 Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu  
           335                          340                          345

gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544  
 Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn  
           350                          355                          360

ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583  
 Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro  
                           365                          370

gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622  
 Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu  
           375                          380                          385

gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661  
 Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu  
                           390                          395

tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700  
 Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro Leu Thr Glu  
           400                          405                          410

gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739  
 Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu  
           415                          420                          425

aga aga aat ggc ttt gga aag aat ggc ttc ttg cag agc 1778  
 Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser  
                           430                          435

cgc agt tcc agt ctg ttc tcc cct tgg aga agc act tgc 1817  
 Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys  
           440                          445                          450

aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856  
 Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser  
                           455                          460

agt gaa aca tca gat gac gat gcc tgg aag t agg 1890  
 Ser Glu Thr Ser Asp Asp Asp Ala Trp Lys  
           465                          470                          474

catataaatg ctacacagtta aatctgaccc aqtaaaactct gtgtgttttag 1940  
 ggagtataca aaagaaatcg ttcttttctt tttcttatgt tgttgaatac 1990  
 ttcattcaca agggaaataa tcatatccca aagagagaaa aaaaaaaaaa 2040  
 aaaggggggc cgcgactcta gqctcgacct gcagtaggga taacagggtg 2090  
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 20 25 30  
 Glu His Leu Pro Arg Gly Glu Gly Arg Phe Gly Val Ser Arg Arg  
 35 40 45  
 Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg  
 50 55 60  
 Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile  
 65 70 75  
 Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln  
 80 85 90  
 Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly  
 95 100 105  
 Met Ser Gln Arg Ser Val Gly Gly Thr Gly Asn His Arg His Trp  
 110 115 120  
 Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys  
 125 130 135  
 Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu  
 140 145 150  
 Lys Leu Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu  
 155 160 165  
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser  
 170 175 180  
 Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met  
 185 190 195  
 Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe  
 200 205 210  
 Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn  
 215 220 225

Lys	Leu	Ser	Ser	Val	Val	Pro	Ser	Val	Tyr	Lys	Asn	Leu	Val	Pro	230	235	240
Lys	Pro	Val	Pro	Pro	Pro	Ser	Lys	Pro	Asn	Ala	Trp	Lys	Ala	Asn	245	250	255
Arg	Met	Glu	His	Lys	Ser	Gly	Ser	Leu	Ser	Ser	Ser	Arg	Glu	Ser	260	265	270
Ala	Phe	Thr	Ser	Pro	Ile	Ser	Val	Thr	Lys	Pro	Val	Val	Leu	Ala	275	280	285
Ser	Gly	Ala	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Ser	Pro	Ser	Ser	Thr	290	295	300
Thr	Pro	Pro	Ile	Glu	Ile	Ser	Ser	Ser	Arg	Leu	Thr	Lys	Leu	Thr	305	310	315
Arg	Arg	Thr	Thr	Asp	Arg	Lys	Ser	Glu	Phe	Leu	Lys	Thr	Leu	Lys	320	325	330
Asp	Asp	Arg	Asn	Gly	Asp	Phe	Ser	Glu	Asn	Arg	Asp	Cys	Asp	Lys	335	340	345
Leu	Glu	Asp	Leu	Glu	Asp	Asn	Ser	Thr	Pro	Glu	Pro	Lys	Glu	Asn	350	355	360
Gly	Glu	Glu	Gly	Cys	His	Gln	Asn	Gly	Leu	Ala	Leu	Pro	Val	Val	365	370	375
Glu	Glu	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Glu	Ala	Glu	His	Arg	380	385	390
Leu	Leu	Lys	Ala	Met	Gly	Trp	Gln	Glu	Tyr	Pro	Glu	Asn	Asp	Glu	395	400	405
Asn	Cys	Leu	Pro	Leu	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Phe	His	Met	410	415	420
Lys	Thr	Glu	Gln	Leu	Arg	Arg	Asn	Gly	Phe	Gly	Lys	Asn	Gly	Phe	425	430	435
Leu	Gln	Ser	Arg	Ser	Ser	Ser	Leu	Phe	Ser	Pro	Trp	Arg	Ser	Thr	440	445	450
Cys	Lys	Ala	Glu	Phe	Glu	Asp	Ser	Asp	Thr	Glu	Thr	Ser	Ser	Ser	455	460	465
Glu	Thr	Ser	Asp	Asp	Asp	Ala	Trp	Lys							470		

<110> 5

<111> 294

<112> DNA

<113> Homo sapiens

<110>

<111> unsure

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 caacacgggtg ccgctgacag cagccatcga ggcgagccag agcctgcagt 100  
 cccacacgga atatattatt cgagtgcaaa gaqqaatttc tctggaaaac 150  
 auctggcaga tngtnagaag atacagtga tlnnatntgc ttaacaacag 200  
 cttncanatt ncaggncna gnnncctct tcttcnaaa aaantgattn 250  
 ggnaacatgg ancgtnant tcatngctng anaggcagnn aggt 294

<210> 6  
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 <213> Homo sapiens

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<210> 7  
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 <212> DNA  
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<210> 9  
 <211> 793  
 <212> DNA  
 <213> Homo sapiens

<210>  
 <211> unsure  
 <222> 379, 433, 459, 492, 517, 541, 549, 561, 575, 579, 582, 710, 742,  
 774, 784  
 <223> unknown base

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 gacctattgg gacaccttct ggagtatggg aaaacccgcc tagtgccaag 150  
 caacctcca agatgctagt tatcaaaaaa gtttccaaag aggatcctgc 200  
 tgctgcyttc tctgctgcat tcacctacc aggatctcac catgcaaagt 250

ggaacaaatt gtcacccgtg gtcccaagtg tctataagaa cctgggttctt 300  
 aagcctgtac caccctcttc caagcctaata gcatggaaag ctaacaggat 350  
 quagpaaag tcaggatccc ttctctctna gccgggagtc tgccttttacc 400  
 attcgaatct ctgttaccaa accagtggtg ctnggctaqt ggtgcagctc 450  
 tcagttctnc ccaaagagag tccctccagc accacccttc cnaattgaga 500  
 tcagctcttc tcgtctngac caagtttgac ccgcggaacc naccgacang 550  
 gaagragtga ngttcctgaa aactnctgna anggatgacc gggaatggga 600  
 agacttityc agaagaatag agactgtgac aagctggaag atttgaggga 650  
 caacagcaca ctgaacaaaa ggaaaatggg ggaggaaggc tgttcatcaa 700  
 atgggtctttn ccttctctgta gttggaagga ggggagggtt tntcacattt 750  
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<210> 10  
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<400> 10  
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<210> 11  
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 <212> DNA  
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<400> 11  
 cccgcctagt gccaaagcaac cctccaagat gctagttatc aaa 43

<210> 12  
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<400> 12  
 cttggtcaga cgagaggagc tgate 25

<210> 13  
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 <212> DNA  
 <213> Homo sapiens

<210>  
 <211> unsure  
 <212> 103  
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<400> 13  
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 agtatgtccc ttctctcacc atg agc tgg etc tcc agt tcc 91

Met Ser Trp Leu Ser Ser Ser  
1 5

cag gga gtg gtn cta aca gcc tac cac ccc agc qgc aag 130  
Gln Gly Val Xaa Leu Thr Ala Tyr His Pro Ser Gly Lys  
10 15 20

gac cag acc gtc qgg aac aqc cat gca aag gca ggg gag 159  
Asp Gln Thr Val Gly Asn Ser His Ala Lys Ala Gly Glu  
25 30

gaa gcc acc tcg agt cgc aga tat ggc cag tac act atg 208  
Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met  
35 40 45

aac cag gaa agc acc acc atc aaa gtt atg gag aag cct 247  
Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro  
50 55

cca ttt gat cga tca att tcc cag gat tct ttg gat gaa 286  
Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu  
60 65 70

cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc 325  
Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile  
75 80 85

aag aaa tct agt gaa aac agc caa gaa gat caa gag gtg 364  
Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val  
90 95

gtt gtt gtc aaa gag cct gat gag gga gaa ttg gaa gaa 403  
Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu  
100 105 110

gag tgg ctt aaa gag gcc ggt tta tcc aat ctc ttc gga 442  
Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly  
115 120

gag tct gct gga gat cca cag gaa agc att gtg ttt tta 481  
Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu  
125 130 135

tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 520  
Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys  
140 145 150

cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac 559  
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn  
155 160

aaa cag tac cag att cct gac gtc aga gac ata ttt gct 598  
Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala  
165 170 175

caa cag aga gaa tca aaa gaa aca gct cca ggt ggc act 637  
Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr  
180 185

gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa 676  
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln

190

195

200

gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag 715  
 Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu  
 205 210 215

aag ctg atc cca cct gag qag acg cct gcc cct gaa aca 754  
 Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr  
 220 225

gac atc aac ctg gag gta tca ttt gcc gag caa qca ctc 793  
 Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu  
 230 235 240

aat cag aaa gag aga tcc aag gag aaa atc cag aag agc 832  
 Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser  
 245 250

aaa gcc gat gat gcc aca tta cct agt ttc aga ttg cca 871  
 Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro  
 255 260 265

aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910  
 Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala  
 270 275 280

ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att 949  
 Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile  
 285 290

gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg 988  
 Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu  
 295 300 305

aaa caa caa aaa gct gtg aaa atc aaa aca aaa gat tct 1027  
 Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser  
 310 315

ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa 1056  
 Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln  
 320 325 330

gat cag agg aaa gta cca gga atg cga ata ccc ttg atc 1105  
 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile  
 335 340 345

ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg 1144  
 Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu  
 350 355

gaa aca gaa gcc ctc tta cgg atc cct gga gct gcc att 1183  
 Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile  
 360 365 370

aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttt 1222  
 Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe  
 375 380

tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat 1261  
 Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His  
 385 390 395

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300  
 Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu  
 400 405 410

ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc ttt 1339  
 Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe  
 415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378  
 Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu  
 425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417  
 Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala  
 440 445

aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456  
 Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln  
 450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495  
 Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val  
 465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534  
 Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met  
 480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573  
 Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu  
 490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612  
 Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu  
 505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651  
 Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys  
 515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690  
 Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn  
 530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729  
 His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys  
 545 550

aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1768  
 Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp  
 555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807  
 Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile  
 570 575

cga gtg caa gct ccc cat ctt tcg aaa gtt tcc atg gca 1846  
 Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala  
 580 585 590

ata aag cta act gaa gaa cta aaa gcc agt gat gta ctt 1885  
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu  
 595 600 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924  
 Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr  
 610 615

ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga gga 1963  
 Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly  
 620 625 630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002  
 Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met  
 635 640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041  
 Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val  
 645 650 655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080  
 Ile Lys Ser Lys Pro Leu  
 660 663

gataaccatg tggacttctg tcataattct tgctgagtca agagtgtaaa 2130  
 taaaagaaat ggcaggactc atattattca gttgtacca agtatttttaa 2180  
 aaatgactct cttaagcctt aaaaagtcac agatttgtgc tgctgccaga 2230  
 attatattaa attattatta atggtattat tagaaaaaaa aatttctgga 2280  
 gtgagagtaa agaggcttaa ttagtttgtg ggcagttttc ttatgctctg 2330  
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 His Pro Ser Gly Lys Asp Gln Thr Val Gly Asn Ser His Ala Lys  
 20 25 30  
 Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr  
 35 40 45  
 Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro  
 50 55 60  
 Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met  
 65 70 75  
 Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu  
 80 85 90  
 Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys Glu Pro Asp

95	100	105
Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly Leu Ser		
110	115	120
Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val		
125	130	135
Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys		
140	145	150
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln		
155	160	165
Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu		
170	175	180
Ser Lys Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg		
185	190	195
Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn		
200	205	210
Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala		
215	220	225
Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala		
230	235	240
Leu Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser Lys		
245	250	255
Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp Lys		
260	265	270
Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys		
275	280	285
Lys Val Cys His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp		
290	295	300
Val Leu Gly Ile Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys		
305	310	315
Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu		
320	325	330
Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile		
335	340	345
Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu Glu Thr		
350	355	360
Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys Asn		
365	370	375
Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn		
380	385	390
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu		
395	400	405

Phe	Ile	Arg	Glu	Leu	Pro	Gln	Pro	Leu	Leu	Ser	Val	Glu	Tyr	Leu	
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Lys	Ala	Phe	Gln	Ala	Val	Gln	Asn	Leu	Pro	Thr	Lys	Lys	Gln	Gln	
				425					430					435	
Leu	Gln	Ala	Leu	Asn	Leu	Leu	Val	Ile	Leu	Leu	Pro	Asp	Ala	Asn	
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Arg	Asp	Thr	Leu	Lys	Ala	Leu	Leu	Glu	Phe	Leu	Gln	Arg	Val	Ile	
				455					460					465	
Asp	Asn	Lys	Glu	Lys	Asn	Lys	Met	Thr	Val	Met	Asn	Val	Ala	Met	
				470					475					480	
Val	Met	Ala	Pro	Asn	Leu	Phe	Met	Cys	His	Ala	Leu	Gly	Leu	Lys	
				485					490					495	
Ser	Ser	Glu	Gln	Arg	Glu	Phe	Val	Met	Ala	Ala	Gly	Thr	Ala	Asn	
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Thr	Met	His	Leu	Leu	Ile	Lys	Tyr	Gln	Lys	Leu	Leu	Trp	Thr	Ile	
				515					520					525	
Pro	Lys	Phe	Ile	Val	Asn	Gln	Val	Arg	Lys	Gln	Asn	Thr	Glu	Asn	
				530					535					540	
His	Lys	Lys	Asp	Lys	Arg	Ala	Met	Lys	Lys	Leu	Leu	Lys	Lys	Met	
				545					550					555	
Ala	Tyr	Asp	Arg	Glu	Lys	Tyr	Glu	Lys	Gln	Asp	Lys	Ser	Thr	Asn	
				560					565					570	
Asp	Ala	Asp	Val	Pro	Gln	Gly	Val	Ile	Arg	Val	Gln	Ala	Pro	His	
				575					580					585	
Leu	Ser	Lys	Val	Ser	Met	Ala	Ile	Gln	Leu	Thr	Glu	Glu	Leu	Lys	
				590					595					600	
Ala	Ser	Asp	Val	Leu	Ala	Arg	Phe	Leu	Ser	Gln	Glu	Ser	Gly	Val	
				605					610					615	
Ala	Gln	Thr	Leu	Lys	Lys	Gly	Glu	Val	Phe	Leu	Tyr	Glu	Ile	Gly	
				620					625					630	
Gly	Asn	Ile	Gly	Glu	Arg	Cys	Leu	Asp	Asp	Asp	Thr	Tyr	Met	Lys	
				635					640					645	
Asp	Leu	Tyr	Gln	Leu	Asn	Pro	Asn	Ala	Glu	Trp	Val	Ile	Lys	Ser	
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Lys Pro Leu

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 <222> 74, 1306  
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 tgcagcaagt ggaggccct gccagcttcg ggctgtggg caggggctca 150  
 ggggggaggg ggtgtggctg ccccgcccg cagcctgca cctgtctct 200  
 cttgtgacc agtaacgcaa ggggatcatc tggggtccg tctgccagga 250

cctgtgtgag ctgcac atg gtg gag tgg agg acc tgc ctc 290  
 Met Val Glu Trp Arg Thr Cys Leu  
 1 5

tgc gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329  
 Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp  
 10 15 20

cgg gac aag gat gta acc atc aag tgt ggc att gag gag 368  
 Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu  
 25 30

acc ctc gac tcc aag gcc cgg tgc gat gcg gcc ccc cgg 407  
 Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg  
 35 40 45

cgg gag ctg gta ctg ttt gac aag ccc acc cgg ggc acc 446  
 Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr  
 50 55 60

tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485  
 Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu  
 65 70

aag gcg aac ctg gga gac ctg cct tcc ctg ccg gcg ctg 524  
 Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu  
 75 80 85

gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563  
 Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp  
 90 95

aac cgg gtc tcc ctg gcg gaa gcc aag tcc gtg tgg gcc 602  
 Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala  
 100 105 110

ctg ctg cag cgt aac gag ttc ctg ctg ctg ctg tcc ctg 641  
 Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Leu Ser Leu  
 115 120 125

cag gag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680  
 Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys  
 130 135

ggg gac ctc tac ctc acc gag ggc gtg ccg cat ggc gcc 719  
 Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

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Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu			
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Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu			
165	170	175	
ggg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc	836		
Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly			
180	185	190	
ctg ctg gag ttc gtg gag gag ctc ttc cag gcc tct tac	875		
Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr			
195	200		
ggg act ttc tac atg tgt gag acc aca ctg gcc aac gtg	914		
Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val			
205	210	215	
ggc tac aca gcc acc tac gac ttc aag atg gcc gac ctg	953		
Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu			
220	225		
cag cag gtg gca ccc gag gcc acc gtg cgc cgc ttc ctg	992		
Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu			
230	235	240	
cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac	1031		
Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr			
245	250	255	
ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg	1070		
Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg			
260	265		
cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag	1109		
Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys			
270	275	280	
gtg tgc gca ctg cta cgg ggc tac ctg ctg cct ggc gcg	1148		
Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala			
285	290		
ccc gcc gac ctc cgc gag gag ctg gcc aca cag ctg cgc	1187		
Pro Ala Asp Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg			
295	300	305	
acc tgt acc acg ctg agc ggg ctg gcc agc cag gtg gag	1226		
Thr Cys Thr Thr Leu Ser Gly Leu Ala Ser Gln Val Glu			
310	315	320	
gcc cat cac tgg ctg gtg ctc agc cac ctc aag act ctg	1265		
Ala His His Ser Leu Val Leu Ser His Leu Lys Thr Leu			
325	330		
ctc tgg aag aag atc tcc aac acc aag tac tct t g	1300		
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335	340	344	

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<213> Homo sapiens

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<222> 104  
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35 40 45  
Pro Arg Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr  
50 55 60  
Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu Lys Ala  
65 70 75  
Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu Val Gly Gln Val  
80 85 90  
Leu Leu Met Ala Asp Phe Asn Lys Asp Asn Arg Val Ser Xaa Ala  
95 100 105  
Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn Glu Phe Leu  
110 115 120  
Leu Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg Leu Leu  
125 130 135  
Gly Tyr Cys Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly  
140 145 150  
Ala Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu Leu  
155 160 165  
Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu Gly Pro Ala  
170 175 180  
Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val  
185 190 195  
Glu Glu Leu Phe His Gly Ser Tyr Gly Thr Phe Tyr Met Cys Glu  
200 205 210  
Thr Thr Leu Ala Asn Val Gly Tyr Thr Ala Thr Tyr Asp Phe Lys  
215 220 225  
Met Ala Asp Leu Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg  
230 235 240

Phe	Leu	Gln	Gly	Arg	Arg	Cys	Glu	His	Ser	Thr	Asp	Cys	Thr	Tyr	245	250	255
Gly	Arg	Asp	Cys	Arg	Ala	Pro	Cys	Asp	Arg	Leu	Met	Arg	Gln	Cys	260	265	270
Lys	Gly	Asp	Leu	Ile	Gln	Pro	Asn	Leu	Ala	Lys	Val	Cys	Ala	Leu	275	280	285
Leu	Arg	Gly	Tyr	Leu	Leu	Pro	Gly	Ala	Pro	Ala	Asp	Leu	Arg	Glu	290	295	300
Glu	Leu	Gly	Thr	Gln	Leu	Arg	Thr	Cys	Thr	Thr	Leu	Ser	Gly	Leu	305	310	315
Ala	Ser	Gln	Val	Glu	Ala	His	His	Ser	Leu	Val	Leu	Ser	His	Leu	320	325	330
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 1924, 1939, 1953, 1982, 1991-1992, 2000, 2443  
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 tgctctngng cncggcaant cnggggagct actgcaccag gggcgctacc 150  
 gggagccctg gcgcgcctg cgaggncctgc gagcagaacc cagtgaactg 200  
 attgtaaaaa ttacagagc ggaatcatat gctggtctcc aagagtttaa 250

agcagcctta	gaagatttaa	atg	cag	ttc	ttt	ttc	aac	ttc	291
		Met	Gln	Phe	Phe	Phe	Asn	Phe	
		1				5			

caa	gat	tgg	cct	gaa	ggt	cta	ctt	cag	gaa	ang	gaa	aaa	330
Gln	Asp	Trp	Pro	Glu	Gly	Leu	Leu	Gln	Glu	Xaa	Glu	Lys	
		10				15						20	

gta	ctc	tgc	gat	gct	ggt	ttt	tta	ggt	gat	gcc	tta	caa	369
Val	Leu	Cys	Asp	Ala	Gly	Phe	Leu	Gly	Asp	Ala	Leu	Gln	
			25						30				

ctc	ttt	ctt	cag	tgc	tta	gcc	ctt	gat	gaa	gat	ttt	gca	408
Leu	Phe	Leu	Gln	Cys	Leu	Ala	Leu	Asp	Glu	Asp	Phe	Ala	
		35				40					45		

cct gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu  
50 55

tta tta cct gaa aac tta aaa gaa ggc ctg aag gaa tct 486  
Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser  
60 65 70

tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525  
Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe  
75 80 85

gat ttt cat tca gtg atg gaa gag tct cag tct ctc aat 564  
Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn  
90 95

gaa cct agc cca aag cag agt gaa gaa ata cca gag gtc 603  
Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val  
100 105 110

act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642  
Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln  
115 120

tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681  
Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg  
125 130 135

gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720  
Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu  
140 145 150

tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759  
Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu  
155 160

tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798  
Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly  
165 170 175

aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837  
Arg Asn Lys Leu Lys Lys Gln Gly Glu Thr Pro Asn Glu  
180 185

gtc tgt atg ttt tcc tta gct tat ggt gat att cca gaa 876  
Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu  
190 195 200

gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915  
Glu Leu Ile Asp Val Ser Asp Phe Glu Cys Ser Leu Cys  
205 210 215

atg agg ttg ttt ttt gag cca gta aca acc cct tgc qqa 954  
Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly  
220 225

cat tgg ttc tgt aag aat tgt ctt gag cgt tgt tta gat 993  
His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp  
230 235 240

cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aat 1032  
His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

gag tat cta gca gat agg agg tac tgt gtc aca cag ctg 1071  
 Glu Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu  
 255 260 265

ttg gaa gaa tta ata gtg aag tat ctg cct gat gaa ctg 1110  
 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu  
 270 275 280

tct gag aga aaa aaa ata tat gaa gaa gaa act gct gaa 1149  
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu  
 285 290

ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188  
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys  
 295 300 305

act atg gcc tac ccc act gtg cct tgc cct ctc cat gta 1227  
 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val  
 310 315

ttt gag cca aga tac aga ttg atg att cga aga agt ata 1265  
 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile  
 320 325 330

cag act gga acc aaa cag ttt ggc atg tgt gtc agt gat 1305  
 Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp  
 335 340 345

aca caa aat agt ttt gca gat tat ggt tgt atg tta caa 1344  
 Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln  
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att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383  
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 360 365 370

gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa 1422  
 Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys  
 375 380

aga gga atg aaa gat gga tat tgc act gcc gac att gaa 1461  
 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu  
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tat ctg gaa gat gtt aag gtt gag aat gaa gat gag att 1500  
 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile  
 400 405 410

aag aat ctc aga gag ctt cat gat ttg gtt tac tct caa 1539  
 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln  
 415 420

gcc tgc agc tgg ttt cag aat tta aga gac aga ttt cga 1578  
 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg  
 425 430 435

agc caa att ctt cag cat ttc gga tca atg ccc gag ang 1617  
 Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Xaa  
 440 445

gag gaa aac ctt cag gca gcc cct aat gga cct gca tgg 1656  
 Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp  
 450 455 460

tgt tgg tgg ctt ctt gca gtt ctc cct gta gac cca cga 1695  
 Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg  
 465 470 475

tac cag ctg tgg gtt ttg tca atg aag tct ttg aaa gaa 1734  
 Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu  
 480 485

cgg ttg acc aag ata cag cat ata ctg acc tat ttt tct 1773  
 Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser  
 490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810  
 Arg Asp Gln Ser Lys  
 505 506

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 tgcgtgctgt tgtgcttgtg ggggttgggt agtgtgtgtg tattttctct 2160  
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 ggggcttttc acattaactg cccatttgtg taatttatag tttgacatga 2660  
 tgtgtttgtt ttaaaaaaaaa atgcatagta taaacctatt aaggatctgg 2710  
 gaaaagagaa gaagttaaat atagaactaa gcttttaag tttgtttttg 2760  
 tttttaattc tggctctcggg gcaaatgtta gttatgcctt attcatatca 2810

cagttagatc accatgetgc aacatgggtt atattcatgc tgccttagaa 2860  
 acttttgtaa ttatttggtg caaatttggt actgtcctta ttaactttct 2910  
 tttatgtaag taatttgtaa aagtttctta aaatttttgc ttttgcttat 2960  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 18, 448  
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                     20                    25                    30  
 Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe  
                     35                    40                    45  
 Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu  
                     50                    55                    60  
 Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser  
                     65                    70                    75  
 Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val  
                     80                    85                    90  
 Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser  
                     95                    100                    105  
 Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu  
                     110                    115                    120  
 Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro  
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 Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu  
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 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu  
                     155                    160                    165  
 Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu  
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 Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu  
                     185                    190                    195  
 Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

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215	220	225
Pro Cys Gly His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu		
230	235	240
Asp His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn Glu		
245	250	255
Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu Leu Glu Glu		
260	265	270
Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu Ser Glu Arg Lys Lys		
275	280	285
Ile Tyr Glu Glu Glu Thr Ala Glu Leu Ser His Leu Thr Lys Asn		
290	295	300
Val Pro Ile Phe Val Cys Thr Met Ala Tyr Pro Thr Val Pro Cys		
305	310	315
Pro Leu His Val Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg		
320	325	330
Ser Ile Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp		
335	340	345
Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln Ile Arg		
350	355	360
Asn Val His Phe Leu Pro Asp Gly Arg Ser Val Val Asp Thr Val		
365	370	375
Gly Gly Lys Arg Phe Arg Val Leu Lys Arg Gly Met Lys Asp Gly		
380	385	390
Tyr Cys Thr Ala Asp Ile Glu Tyr Leu Glu Asp Val Lys Val Glu		
395	400	405
Asn Glu Asp Glu Ile Lys Asn Leu Arg Glu Leu His Asp Leu Val		
410	415	420
Tyr Ser Gln Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe		
425	430	435
Arg Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Xaa Arg Glu		
440	445	450
Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp Cys Trp Trp		
455	460	465
Leu Leu Ala Val Leu Pro Val Asp Pro Arg Tyr Gln Leu Ser Val		
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Leu Ser Met Lys Ser Leu Lys Glu Arg Leu Thr Lys Ile Gln His		
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Ile Leu Thr Tyr Phe Ser Arg Asp Gln Ser Lys		
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tcagtgtgga gtatctcaaa gcctttcagg ctgtccagaa ttttccaacc 200  
aagaagcagc aactacaggg cttttgaacc ctttctttta ctcatcctg 250  
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cctggccaac cagcgccggc aggggaaggca ggtctcccag gttcgccttg 150  
aggaagccga gggtcacctc ccggaattcc ttgatggagg tgccccgggt 200  
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cttggagtgc agggctctct caatgccaca cttgatgggt acatccttgt 300  
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09/684,458

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PRO-C-MG.12	SEQ ID 3	SEQ ID 4
PRO-C-MG.45	SEQ ID 17	SEQ ID 18
PRO-C-MG.64	SEQ ID 15	SEQ ID 16
PRO-C-MG.72	SEQ ID 13	SEQ ID 14